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SEP 08 2003

TECH CENTER 1600



1600

RAW SEQUENCE LISTING

DATE: 08/29/2003

PATENT APPLICATION: US/09/578,900B

TIME: 15:29:16

Input Set : A:\03-08-23 032796-019.ST25.txt

Output Set: N:\CRF4\08292003\I578900B.raw

4 <110> APPLICANT: Carulli, John P.
 5 Little, Randall D.
 6 Recker, Robert R.
 7 Johnson, Mark L.
 9 <120> TITLE OF INVENTION: REGULATING LIPID LEVELS VIA THE ZMAX1 OR HBM GENE
 11 <130> FILE REFERENCE: 032796-019
 13 <140> CURRENT APPLICATION NUMBER: US 09/578,900B
 14 <141> CURRENT FILING DATE: 2000-05-26
 16 <150> PRIOR APPLICATION NUMBER: US 09/543,771
 17 <151> PRIOR FILING DATE: 2000-04-05
 19 <150> PRIOR APPLICATION NUMBER: US 09/229,319
 20 <151> PRIOR FILING DATE: 1999-01-13
 22 <150> PRIOR APPLICATION NUMBER: US 60/071,449
 23 <151> PRIOR FILING DATE: 1998-01-13
 25 <150> PRIOR APPLICATION NUMBER: US 60/105,511
 26 <151> PRIOR FILING DATE: 1998-10-23
 28 <160> NUMBER OF SEQ ID NOS: 641
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 5120
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <400> SEQUENCE: 1

37 actaaagcgc cgccgcgcgc ccatggagcc cgagtgcgcg cggcgcgggc ccgtccggcc 60
 38 gccggacaac atg gag gca gcg ccg ccc ggg ccg ccg tgg ccg ctg ctg 109
 39 Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
 40 1 5 10
 41 ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc 157
 42 Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
 43 15 20 25
 44 gcg gcc tcg ccg ctc ctg cta ttt gcc aac cgc cgg gac gta cgg ctg 205
 45 Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
 46 30 35 40 45
 47 gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc 253
 48 Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
 49 50 55 60
 50 ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
 51 Leu Glu Asp Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
 52 65 70 75
 53 tac tgg aca gac gtg agc gag gag gcc atc aag cag acc tac ctg aac 349
 54 Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
 55 80 85 90
 56 cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct 397
 57 Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser

pb
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58	95	100	105	
59	ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg	445		
60	Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr			
61	110 115 120 125			
62	gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc	493		
63	Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser			
64	130 135 140			
65	cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc	541		
66	Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala			
67	145 150 155			
68	ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg ggt gag acg	589		
69	Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr			
70	160 165 170			
71	ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att	637		
72	Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile			
73	175 180 185			
74	gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag	685		
75	Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu			
76	190 195 200 205			
77	gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt	733		
78	Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg			
79	210 215 220			
80	gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg	781		
81	Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu			
82	225 230 235			
83	acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca	829		
84	Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr			
85	240 245 250			
86	gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg	877		
87	Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly			
88	255 260 265			
89	aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag	925		
90	Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln			
91	270 275 280 285			
92	gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag	973		
93	Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu			
94	290 295 300			
95	gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct	1021		
96	Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro			
97	305 310 315			
98	ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc	1069		
99	Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly			
100	320 325 330			
101	agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg	1117		
102	Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg			
103	335 340 345			
104	acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc	1165		
105	Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile			
106	350 355 360 365			

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107	gtg	ctg	cag	gtg	gac	gac	atc	cgg	cac	gcc	att	gcc	atc	gac	tac	gac	1213
108	Val	Leu	Gln	Val	Asp	Asp	Ile	Arg	His	Ala	Ile	Ala	Ile	Asp	Tyr	Asp	
109					370					375					380		
110	ccg	cta	gag	ggc	tat	gtc	tac	tgg	aca	gat	gac	gag	gtg	cgg	gcc	atc	1261
111	Pro	Leu	Glu	Gly	Tyr	Val	Tyr	Trp	Thr	Asp	Asp	Glu	Val	Arg	Ala	Ile	
112				385						390					395		
113	cgc	agg	gcg	tac	ctg	gac	ggg	tct	ggg	gcg	cag	acg	ctg	gtc	aac	acc	1309
114	Arg	Arg	Ala	Tyr	Leu	Asp	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Val	Asn	Thr	
115			400					405						410			
116	gag	atc	aac	gac	ccc	gat	ggc	atc	gcg	gtc	gac	tgg	gtg	gcc	cga	aac	1357
117	Glu	Ile	Asn	Asp	Pro	Asp	Gly	Ile	Ala	Val	Asp	Trp	Val	Ala	Arg	Asn	
118		415					420					425					
119	ctc	tac	tgg	acc	gac	acg	ggc	acg	gac	cgc	atc	gag	gtg	acg	cgc	ctc	1405
120	Leu	Tyr	Trp	Thr	Asp	Thr	Gly	Thr	Asp	Arg	Ile	Glu	Val	Thr	Arg	Leu	
121	430						435					440				445	
122	aac	ggc	acc	tcc	cgc	aag	atc	ctg	gtg	tcg	gag	gac	ctg	gac	gag	ccc	1453
123	Asn	Gly	Thr	Ser	Arg	Lys	Ile	Leu	Val	Ser	Glu	Asp	Leu	Asp	Glu	Pro	
124				450						455					460		
125	cga	gcc	atc	gca	ctg	cac	ccc	gtg	atg	ggc	ctc	atg	tac	tgg	aca	gac	1501
126	Arg	Ala	Ile	Ala	Leu	His	Pro	Val	Met	Gly	Leu	Met	Tyr	Trp	Thr	Asp	
127				465						470					475		
128	tgg	gga	gag	aac	cct	aaa	atc	gag	tgt	gcc	aac	ttg	gat	ggg	cag	gag	1549
129	Trp	Gly	Glu	Asn	Pro	Lys	Ile	Glu	Cys	Ala	Asn	Leu	Asp	Gly	Gln	Glu	
130			480					485						490			
131	cgg	cgt	gtg	ctg	gtc	aat	gcc	tcc	ctc	ggg	tgg	ccc	aac	ggc	ctg	gcc	1597
132	Arg	Arg	Val	Leu	Val	Asn	Ala	Ser	Leu	Gly	Trp	Pro	Asn	Gly	Leu	Ala	
133		495					500							505			
134	ctg	gac	ctg	cag	gag	ggg	aag	ctc	tac	tgg	gga	gac	gcc	aag	aca	gac	1645
135	Leu	Asp	Leu	Gln	Glu	Gly	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Lys	Thr	Asp	
136	510					515					520					525	
137	aag	atc	gag	gtg	atc	aat	gtt	gat	ggg	acg	aag	agg	cgg	acc	ctc	ctg	1693
138	Lys	Ile	Glu	Val	Ile	Asn	Val	Asp	Gly	Thr	Lys	Arg	Arg	Thr	Leu	Leu	
139				530						535					540		
140	gag	gac	aag	ctc	cgg	cac	att	ttc	ggg	ttc	acg	ctg	ctg	ggg	gac	ttc	1741
141	Glu	Asp	Lys	Leu	Pro	His	Ile	Phe	Gly	Phe	Thr	Leu	Leu	Gly	Asp	Phe	
142			545							550					555		
143	atc	tac	tgg	act	gac	tgg	cag	cgc	cgc	agc	atc	gag	cgg	gtg	cac	aag	1789
144	Ile	Tyr	Trp	Thr	Asp	Trp	Gln	Arg	Arg	Ser	Ile	Glu	Arg	Val	His	Lys	
145			560					565						570			
146	gtc	aag	gcc	agc	cgg	gac	gtc	atc	att	gac	cag	ctg	ccc	gac	ctg	atg	1837
147	Val	Lys	Ala	Ser	Arg	Asp	Val	Ile	Ile	Asp	Gln	Leu	Pro	Asp	Leu	Met	
148		575					580							585			
149	ggg	ctc	aaa	gct	gtg	aat	gtg	gcc	aag	gtc	gtc	gga	acc	aac	cgg	tgt	1885
150	Gly	Leu	Lys	Ala	Val	Asn	Val	Ala	Lys	Val	Val	Gly	Thr	Asn	Pro	Cys	
151	590					595					600					605	
152	gcg	gac	agg	aac	ggg	ggg	tgc	agc	cac	ctg	tgc	ttc	ttc	aca	ccc	cac	1933
153	Ala	Asp	Arg	Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Phe	Phe	Thr	Pro	His	
154				610						615					620		
155	gca	acc	cgg	tgt	ggc	tgc	ccc	atc	ggc	ctg	gag	ctg	ctg	agt	gac	atg	1981

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156	Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met	
157	625 630 635	
158	aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc	2029
159	Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala	
160	640 645 650	
161	gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc	2077
162	Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile	
163	655 660 665	
164	ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc	2125
165	Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser	
166	670 675 680 685	
167	aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc	2173
168	Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg	
169	690 695 700	
170	gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt	2221
171	Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu	
172	705 710 715	
173	gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac	2269
174	Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr	
175	720 725 730	
176	tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg	2317
177	Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly	
178	735 740 745	
179	cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg	2365
180	Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser	
181	750 755 760 765	
182	ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc	2413
183	Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly	
184	770 775 780	
185	ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg	2461
186	Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met	
187	785 790 795	
188	acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac	2509
189	Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr	
190	800 805 810	
191	gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag	2557
192	Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu	
193	815 820 825	
194	tcg tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc	2605
195	Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu	
196	830 835 840 845	
197	ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca	2653
198	Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr	
199	850 855 860	
200	gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg	2701
201	Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg	
202	865 870 875	
203	aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg	2749
204	Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu	

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205		880		885		890		
206	gtg	ttc	cac	tcc	tcc	cgc	cag	gat
207	Val	Phe	His	Ser	Ser	Arg	Gln	Asp
208		895		900		905		
209	aac	ggg	cag	tgt	ggg	cag	ctg	tgc
210	Asn	Gly	Gln	Cys	Gly	Gln	Leu	Cys
211	910			915		920		925
212	tgc	ggc	tgc	gcc	tca	cac	tac	acc
213	Cys	Gly	Cys	Ala	Ser	His	Tyr	Thr
214				930		935		940
215	agc	ccg	ccc	acc	acc	ttc	ttg	ctg
216	Ser	Pro	Pro	Thr	Thr	Phe	Leu	Leu
217				945		950		955
218	cgg	atg	atc	ccg	gac	gac	cag	cac
219	Arg	Met	Ile	Pro	Asp	Asp	Gln	His
220				960		965		970
221	cat	gga	ctg	agg	aac	gtc	aaa	gcc
222	His	Gly	Leu	Arg	Asn	Val	Lys	Ala
223				975		980		985
224	ttc	atc	tac	tgg	gtg	gat	ggg	cgc
225	Phe	Ile	Tyr	Trp	Val	Asp	Gly	Arg
226	990			995		1000		1005
227	gac	ggg	acc	cag	ccc	ttt	gtt	ttg
228	Asp	Gly	Thr	Gln	Pro	Phe	Val	Leu
229				1010		1015		1020
230	cca	gac	agg	cag	ccc	cac	gac	ctc
231	Pro	Asp	Arg	Gln	Pro	His	Asp	Leu
232				1025		1030		1035
233	ctg	ttc	tgg	acg	tgc	gag	gcc	acc
234	Leu	Phe	Trp	Thr	Cys	Glu	Ala	Thr
235				1040		1045		1050
236	agc	ggg	gaa	gcc	atg	ggg	gtg	gtg
237	Ser	Gly	Glu	Ala	Met	Gly	Val	Val
238				1055		1060		1065
239	agg	gcc	atc	gtc	gtc	aac	gcg	gag
240	Arg	Ala	Ile	Val	Val	Asn	Ala	Glu
241	1070			1075		1080		1085
242	atg	cag	gac	cgg	gca	gcc	aag	atc
243	Met	Gln	Asp	Arg	Ala	Ala	Lys	Ile
244				1090		1095		1100
245	gag	cgc	gag	gtc	ctc	ttc	acc	acc
246	Glu	Arg	Glu	Val	Leu	Phe	Thr	Thr
247				1105		1110		1115
248	gtg	gtg	gac	aac	aca	ctg	ggc	aag
249	Val	Val	Asp	Asn	Thr	Leu	Gly	Lys
250				1120		1125		1130
251	aag	cgc	att	gag	agc	tgt	gac	ctg
252	Lys	Arg	Ile	Glu	Ser	Cys	Asp	Leu
253				1135		1140		1145

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 12044,12489,26433,26434,26435,26436,26439,26441

Seq#:7; N Pos. 4336,4345,4349,4392,4447,4490

Seq#:8; N Pos. 33739,33749,33758

Seq#:9; N Pos. 8356,8385,38585

Seq#:176; N Pos. 12

Seq#:268; N Pos. 8